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2350-Pos Board B487
Molecular Models of Nanodiscs for Studying Membrane Proteins
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In recent years an engineered form of discoloidal high-density lipoprotein particle, called nanodisc, has been proposed as a platform to study membrane proteins. A nanodisc is a non-covalent assembly of phospholipids and two membrane scaffold proteins which wrap around the bilayer, shielding the phospholipids' hydrophobic alkyl chains from the aqueous environment. During the reconstitution process a membrane protein is simultaneously assembled into the nanodisc core. The nanodisc forms a soluble lipid bilayer that enables membrane protein function and stability in solution while also preventing unwanted aggregation.
In this work we present an automated method for building arbitrary nanodiscs and example applications to membrane proteins from different families. We use the MARTINI coarse-grained (CG) force field with the elastic network model ELNEDYN to generate initial configurations of membrane protein-loaded nanodiscs, where the size and composition of the system is fully controlled. The system can be studied using either CG molecular dynamics simulations to analyze properties like lipid mixing and packing in the nanodiscs, or back-mapped after equilibration to an atomistic resolution for more detailed analyses.

2351-Pos Board B488
Influence of Yersinia Pestis Lipopolysaccharide Structure upon Outer Membrane Dynamics: Insight from Molecular Dynamics Simulations
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Yersinia pestis, the causative agent of plague, is not only still prevalent in many different parts of the world but is also classified as a potential biological warfare agent. Y. pestis is a Gram-negative bacterium and is therefore surrounded by two membranes. The outer of these two membranes is arranged with an asymmetric lipid distribution; phospholipids comprise the inner leaflet of the membrane, while the outer leaflet contains the complex glycolipid lipopolysaccharide (LPS). Not only is this outer membrane important in functioning as the first barrier that molecules must cross to enter the bacterial cell but also because it is a potential target for antimicrobial drugs. The LPS within the outer membrane of Y. pestis is unusual in the fact that it undergoes substantial, temperature-dependent, structural variation. This temperature dependence of the LPS structure is important in both resistance to antimicrobial peptides and the ability to evade the human innate immune system.
In this presented work, we aimed to explore the details of the molecular interactions which govern the properties of the outer membrane of Y. pestis. In particular, atomistic models for the different temperature-dependent structural variations of the LPS have been constructed. Subsequent molecular dynamics simulations have elucidated the impact of these structural changes upon the properties of the outer membrane. Finally the impact of the addition of a cationic monosaccharide to lipid A, a common structural variant that increases the resistance of Y. pestis to cationic antimicrobial peptides, has also been explored through molecular simulation.

2352-Pos Board B489
Computational Studies of Nile Red in Lipid Bilayers
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The dye 9-diethylamino-5H-benzo[α]phenoxazine-5-one, commonly known as Nile Red, is a fluorescent molecule whose position of excitation and emission maxima are dependent on the polarity of the solvent. The dye is mainly used as a probe for the determination of the lipid microenvironment.
In this presentation we discuss the development of a methodology for the prediction of the optical shifts of Nile Red in various lipid bilayer environments. This approach incorporates: 1) development of an improved MM model of Nile Red, 2) Potential of Mean Force (PMF) calculations to determine the orientation and position of the dye in the bilayer, 3) clustering to identify representative configurations and 4) combined QM/MM calculations to predict the spectra of each selected configuration of Nile Red in a bilayer. We will also present preliminary results highlighting the application of the newly developed methodology.

2353-Pos Board B490
Molecular Dynamics Studies for the Sugar Transportation Mechanism in Phosphotransferase Systems (PTSS)
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All living organisms not only need saccharides as nutrition but also use them as recognition markers by forming glycoconjugates. Therefore, a set of processes for sugar transport into the cell through the membrane is necessary for living cells. In bacteria, it is well known that sugar is transported into cytosol through the cell membrane by phosphoenolpyruvate-dependent phosphotransferase systems (PTSs). However, the detailed mechanism of how PTSs transport sugar through the cell membrane is still elusive. In 2011, Cao et al. first determined the crystal structure of an occluded state of membrane protein EIIC, which is the most important component in PTSs, of chitobiose-specific PTS. Even though the crystal structure can be used to suggest potential sugar transportation mechanisms, structural information of outward-open or inward-open states are needed to identify the correct mechanism. In this study, we model the plausible structures of outward-open states of EIIC by performing three independent rigid-body rotation molecular dynamics simulations in explicit membranes. Our model structures provide several key points that stabilize the outward-open states and give insights into the saccharide transport mechanism. This study could be a base for finding the reasonable mechanism of the saccharide transport and further experiments.

2354-Pos Board B491
Effect of Asymmetry on Bilayer Membrane Systems
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Many biological processes, such as membrane fusion and the action of microbial proteins, involve asymmetric uptake of proteins. In addition, it has been demonstrated that large mechaosensitive channels open by the asymmetric inclusion of lyso-lipids in the bilayer in the absence of external pressure. These phenomena can be interpreted in terms of the asymmetric local pressure profile in the bilayer, which lacks the quantitative understanding. By noting that such asymmetric pressure profile can be induced in bilayer membranes with asymmetric number of lipids between leaflets, to provide quantitative understanding, we performed molecular dynamics simulations of 1,2-dimyristoyl-*sn*-glycero-3-phosphocholine (DMPC) and 1-palmitoyl-2-oleoylphosphatidylcholine (POPC) bilayer membranes for a set of systems with different level of asymmetry with and without gramicidin A (gA) or WALP23. We observed that even highly asymmetric lipid bilayers with and without gA or WALP23 were stable during the whole simulation time, which is consistent with the previous study of dipalmitoyl-phosphatidylcholine (DPPC) bilayers [*J. Am. Chem. Soc.* **131**, 15194 (2009)]. As the number of lipids in the lower leaflet becomes smaller, the lipids are more tightly packed in the top leaflet and less ordered in the bottom leaflet, which are quantified in terms the lateral pressure profile, the order parameter, the area per lipid, etc. However, the hydrophobic thickness for pure lipid bilayers does not show meaningful dependence on the asymmetry, which results from the stretched and less ordered lipids in the upper and lower leaflets, respectively. We will also discuss the influence of the asymmetry on the properties of protein-lipid interactions, such as the distance dependence of the lipid properties and the interaction patterns around gA or WALP23.

2355-Pos Board B492
Conformational Dynamics of Phus
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Iron is essential for pathogen's survival and virulence in the host and it requires specialized mechanisms for uptake and storage. PhuS is a cytoplasmic heme-trafficking protein in the opportunistic Gram-negative pathogen Pseudomonas aeruginosa. Heme binding to PhuS has been thought to occur by an induced-fit mechanism. However, this assumption is recently challenged by the structure of the holo form, which shows no significant difference from the apo form. To resolve the controversy, we performed molecular dynamics simulation of the apo form of PhuS. We found that the apo PhuS samples a conformational space distinct from the holo structure, thus providing new insights into the mechanism of heme trafficking in P. aeruginosa.

2356-Pos Board B493
Aquaporin-0 Water Conduction Regulation by Calmodulin
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Aquaporin-0 (AQP0) contributes to the nurturing and cleaning of the eye lens of waste product. It is a tetrameric protein composed of four identical